

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT:
(A) NAME: Kossmann, Jens
Buttcher, Volker
Welsh, Thomas
- (ii) TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES CAPABLE
OF FACILITATING THE SYNTHESIS OF LINEAR
ALPHA-1,4 GLUCANS IN PLANTS, FUNGI AND
MICROORGANISMS
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave
(B) STREET: 1251 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: United States of America
(F) ZIP: 10020
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: DE P 44 17 879.4
(B) FILING DATE: 18-MAY-1994
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: DE P 44 47 388.5
(B) FILING DATE: 22-DEC-1994
- (vii) ATTORNEY/AGENT INFORMATION:
(A) NAME: James F. Haley, Jr., Esq.
(B) REGISTRATION NUMBER: 27,794
(C) DOCKET NUMBER: GFB-1
- (viii) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 596-9000
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(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2914 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria polysaccharea*

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: genomic library in pBluescriptII SK

(B) CLONE: pNB2

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 957..2867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GAGTTTTGCG TTCCCGAACC GAACGTGATG CTTGAGCCGA ACACCTGTCC GGCAAGGCGG	60
CTGACCGCCC CCTTTTGCCC CATCGACATC GTAACAATCG GTTTGGTGGC AAGCTCTTTC	120
GCTTTGAGCG TGGCAGAAAG CAAAGTCAGC ACGTCTTCCG CGCTTTGCGG CATCACCGCA	180
ATTTTGCAGA TGTCCGCGCC GCAGTCCTCC ATCTGTTTCA GACGGCATA CATTCTTCT	240
TGCGGCGGCG TGCGGTGAAA CTCATGATTG CAGAGCAGGG CGGCGATGCC GTTTTTTTGA	300
GCATGCGCCA CGGCGCGCCG GACGGCGGTT TCGCCGGAAA AAAGCTCGAT ATCGATAATG	360
TCGGGCAGGC GGCTTTCAAT CAGCGAGTCG AGCAGTTCAA AATAATAATC GTCCGAACAC	420
GGGAACGAGC CGCCTTCGCC ATGCCGTCTG AACGTAAACA GCAGCGGCTT GTCGGGCAGC	480
GCGTCGCGGA CGGTCTGCGT GTGGCGCAAT ACTTCGCCGA TGCTGCCCCG GCATTCCAAA	540
AAATCGGCGC GGAACTCGAC GATATCGAAG GGCAGGTTTT TGATTTGGTC AAGTACGGCG	600
GAAAGTACGG CGGCATCGCG GCGACAAGC GGCACGGCGA TTTTGGTGCG TCCGCTTCCG	660
ATAACGGTGT TTTTGACGGT CAGGCTGGTG TGCATGGCGG TTGTTGCGGC TGAAAGGAAC	720
GGTAAAGACG CAATTATAGC AAAGGCACAG GCAATGTTTC AGACGGCATT TCTGTGCGGC	780
CGGCTTGATA TGAATCAAGC AGCATCCGCA TATCGGAATG CAGACTTGGC ACAAGCCCTG	840
TCTTTTCTAG TCAGTCCGCA GTTCTTGCGA TATGATTGCA CGACACGCCC TACACGGCAT	900
TTGCAGGATA CGGCGGCAGA CCGCCGGTCG GAAACTTCAG AATCGGAGCA GGCATC	956
ATG TTG ACC CCC ACG CAG CAA GTC GGT TTG ATT TTA CAG TAC CTC AAA	1004
Met Leu Thr Pro Thr Gln Gln Val Gly Leu Ile Leu Gln Tyr Leu Lys	
1 5 10 15	
ACA CGC ATC TTG GAC ATC TAC ACG CCC GAA CAG CGC GCC GGC ATC GAA	1052
Thr Arg Ile Leu Asp Ile Tyr Thr Pro Glu Gln Arg Ala Gly Ile Glu	
20 25 30	
AAA TCC GAA GAC TGG CGG CAG TTT TCG CGC CGC ATG GAT ACG CAT TTC	1100

Lys	Ser	Glu	Asp	Trp	Arg	Gln	Phe	Ser	Arg	Arg	Met	Asp	Thr	His	Phe	
		35					40					45				
CCC	AAA	CTG	ATG	AAC	GAA	CTC	GAC	AGC	GTG	TAC	GGC	AAC	AAC	GAA	GCC	1148
Pro	Lys	Leu	Met	Asn	Glu	Leu	Asp	Ser	Val	Tyr	Gly	Asn	Asn	Glu	Ala	
	50					55					60					
CTG	CTG	CCT	ATG	CTG	GAA	ATG	CTG	CTG	GCG	CAG	GCA	TGG	CAA	AGC	TAT	1196
Leu	Leu	Pro	Met	Leu	Glu	Met	Leu	Leu	Ala	Gln	Ala	Trp	Gln	Ser	Tyr	
	65				70					75					80	
TCC	CAA	CGC	AAC	TCA	TCC	TTA	AAA	GAT	ATC	GAT	ATC	GCG	CGC	GAA	AAC	1244
Ser	Gln	Arg	Asn	Ser	Ser	Leu	Lys	Asp	Ile	Asp	Ile	Ala	Arg	Glu	Asn	
				85					90					95		
AAC	CCC	GAT	TGG	ATT	TTG	TCC	AAC	AAA	CAA	GTC	GGC	GGC	GTG	TGC	TAC	1292
Asn	Pro	Asp	Trp	Ile	Leu	Ser	Asn	Lys	Gln	Val	Gly	Gly	Val	Cys	Tyr	
		100						105					110			
GTT	GAT	TTG	TTT	GCC	GGC	GAT	TTG	AAG	GGC	TTG	AAA	GAT	AAA	ATT	CCT	1340
Val	Asp	Leu	Phe	Ala	Gly	Asp	Leu	Lys	Gly	Leu	Lys	Asp	Lys	Ile	Pro	
		115					120						125			
TAT	TTT	CAA	GAG	CTT	GGT	TTG	ACT	TAT	CTG	CAC	CTG	ATG	CCG	CTG	TTT	1388
Tyr	Phe	Gln	Glu	Leu	Gly	Leu	Thr	Tyr	Leu	His	Leu	Met	Pro	Leu	Phe	
	130					135					140					
AAA	TGC	CCT	GAA	GGC	AAA	AGC	GAC	GGC	GGC	TAT	GCG	GTC	AGC	AGC	TAC	1436
Lys	Cys	Pro	Glu	Gly	Lys	Ser	Asp	Gly	Gly	Tyr	Ala	Val	Ser	Ser	Tyr	
	145				150					155					160	
CGC	GAT	GTC	AAT	CCG	GCA	CTG	GGC	ACA	ATA	GGC	GAC	TTG	CGC	GAA	GTC	1484
Arg	Asp	Val	Asn	Pro	Ala	Leu	Gly	Thr	Ile	Gly	Asp	Leu	Arg	Glu	Val	
				165					170					175		
ATT	GCT	GCG	CTG	CAC	GAA	GCC	GGC	ATT	TCC	GCC	GTC	GTC	GAT	TTT	ATC	1532
Ile	Ala	Ala	Leu	His	Glu	Ala	Gly	Ile	Ser	Ala	Val	Val	Asp	Phe	Ile	
			180				185						190			
TTC	AAC	CAC	ACC	TCC	AAC	GAA	CAC	GAA	TGG	GCG	CAA	CGC	TGC	GCC	GCC	1580
Phe	Asn	His	Thr	Ser	Asn	Glu	His	Glu	Trp	Ala	Gln	Arg	Cys	Ala	Ala	
		195					200					205				
GGC	GAC	CCG	CTT	TTC	GAC	AAT	TTC	TAC	TAT	ATT	TTC	CCC	GAC	CGC	CGG	1628
Gly	Asp	Pro	Leu	Phe	Asp	Asn	Phe	Tyr	Tyr	Ile	Phe	Pro	Asp	Arg	Arg	
	210					215					220					
ATG	CCC	GAC	CAA	TAC	GAC	CGC	ACC	CTG	CGC	GAA	ATC	TTC	CCC	GAC	CAG	1676
Met	Pro	Asp	Gln	Tyr	Asp	Arg	Thr	Leu	Arg	Glu	Ile	Phe	Pro	Asp	Gln	
	225				230					235					240	
CAC	CCG	GGC	GGC	TTC	TCG	CAA	CTG	GAA	GAC	GGA	CGC	TGG	GTG	TGG	ACG	1724
His	Pro	Gly	Gly	Phe	Ser	Gln	Leu	Glu	Asp	Gly	Arg	Trp	Val	Trp	Thr	
				245					250					255		
ACC	TTC	AAT	TCC	TTC	CAA	TGG	GAC	TTG	AAT	TAC	AGC	AAC	CCG	TGG	GTA	1772
Thr	Phe	Asn	Ser	Phe	Gln	Trp	Asp	Leu	Asn	Tyr	Ser	Asn	Pro	Trp	Val	
			260					265					270			

TTC CGC GCA ATG GCG GGC GAA ATG CTG TTC CTT GCC AAC TTG GGC GTT Phe Arg Ala Met Ala Gly Glu Met Leu Phe Leu Ala Asn Leu Gly Val 275 280 285	1820
GAC ATC CTG CGT ATG GAT GCG GTT GCC TTT ATT TGG AAA CAA ATG GGG Asp Ile Leu Arg Met Asp Ala Val Ala Phe Ile Trp Lys Gln Met Gly 290 295 300	1868
ACA AGC TGC GAA AAC CTG CCG CAG GCG CAC GCC CTC ATC CGC GCG TTC Thr Ser Cys Glu Asn Leu Pro Gln Ala His Ala Leu Ile Arg Ala Phe 305 310 315 320	1916
AAT GCC GTT ATG CGT ATT GCC GCG CCC GCC GTG TTC TTC AAA TCC GAA Asn Ala Val Met Arg Ile Ala Ala Pro Ala Val Phe Phe Lys Ser Glu 325 330 335	1964
GCC ATC GTC CAC CCC GAC CAA GTC GTC CAA TAC ATC GGG CAG GAC GAA Ala Ile Val His Pro Asp Gln Val Val Gln Tyr Ile Gly Gln Asp Glu 340 345 350	2012
TGC CAA ATC GGT TAC AAC CCC CTG CAA ATG GCA TTG TTG TGG AAC ACC Cys Gln Ile Gly Tyr Asn Pro Leu Gln Met Ala Leu Leu Trp Asn Thr 355 360 365	2060
CTT GCC ACG CGC GAA GTC AAC CTG CTC CAT CAG GCG CTG ACC TAC CGC Leu Ala Thr Arg Glu Val Asn Leu Leu His Gln Ala Leu Thr Tyr Arg 370 375 380	2108
CAC AAC CTG CCC GAG CAT ACC GCC TGG GTC AAC TAC GTC CGC AGC CAC His Asn Leu Pro Glu His Thr Ala Trp Val Asn Tyr Val Arg Ser His 385 390 395 400	2156
GAC GAC ATC GGC TGG ACG TTT GCC GAT GAA GAC GCG GCA TAT CTG GGC Asp Asp Ile Gly Trp Thr Phe Ala Asp Glu Asp Ala Ala Tyr Leu Gly 405 410 415	2204
ATA AGC GGC TAC GAC CAC CGC CAA TTC CTC AAC CGC TTC TTC GTC AAC Ile Ser Gly Tyr Asp His Arg Gln Phe Leu Asn Arg Phe Phe Val Asn 420 425 430	2252
CGT TTC GAC GGC AGC TTC GCT CGT GGC GTA CCG TTC CAA TAC AAC CCA Arg Phe Asp Gly Ser Phe Ala Arg Gly Val Pro Phe Gln Tyr Asn Pro 435 440 445	2300
AGC ACA GGC GAC TGC CGT GTC AGT GGT ACA GCC GCG GCA TTG GTC GGC Ser Thr Gly Asp Cys Arg Val Ser Gly Thr Ala Ala Ala Leu Val Gly 450 455 460	2348
TTG GCG CAA GAC GAT CCC CAC GCC GTT GAC CGC ATC AAA CTC TTG TAC Leu Ala Gln Asp Asp Pro His Ala Val Asp Arg Ile Lys Leu Leu Tyr 465 470 475 480	2396
AGC ATT GCT TTG AGT ACC GGC GGT CTG CCG CTG ATT TAC CTA GGC GAC Ser Ile Ala Leu Ser Thr Gly Gly Leu Pro Leu Ile Tyr Leu Gly Asp 485 490 495	2444
GAA GTG GGT ACG CTC AAT GAC GAC GAC TGG TCG CAA GAC AGC AAT AAG Glu Val Gly Thr Leu Asn Asp Asp Asp Trp Ser Gln Asp Ser Asn Lys 500 505 510	2492

AGC GAC GAC AGC CGT TGG GCG CAC CGT CCG CGC TAC AAC GAA GCC CTG	2540
Ser Asp Asp Ser Arg Trp Ala His Arg Pro Arg Tyr Asn Glu Ala Leu	
515 520 525	
TAC GCG CAA CGC AAC GAT CCG TCG ACC GCA GCC GGG CAA ATC TAT CAG	2588
Tyr Ala Gln Arg Asn Asp Pro Ser Thr Ala Ala Gly Gln Ile Tyr Gln	
530 535 540	
GGC TTG CGC CAT ATG ATT GCC GTC CGC CAA AGC AAT CCG CGC TTC GAC	2636
Gly Leu Arg His Met Ile Ala Val Arg Gln Ser Asn Pro Arg Phe Asp	
545 550 555 560	
GGC GGC AGG CTG GTT ACA TTC AAC ACC AAC AAC AAG CAC ATC ATC GGC	2684
Gly Gly Arg Leu Val Thr Phe Asn Thr Asn Asn Lys His Ile Ile Gly	
565 570 575	
TAC ATC CGC AAC AAT GCG CTT TTG GCA TTC GGT AAC TTC AGC GAA TAT	2732
Tyr Ile Arg Asn Asn Ala Leu Leu Ala Phe Gly Asn Phe Ser Glu Tyr	
580 585 590	
CCG CAA ACC GTT ACC GCG CAT ACC CTG CAA GCC ATG CCC TTC AAG GCG	2780
Pro Gln Thr Val Thr Ala His Thr Leu Gln Ala Met Pro Phe Lys Ala	
595 600 605	
CAC GAC CTC ATC GGT GGC AAA ACT GTC AGC CTG AAT CAG GAT TTG ACG	2828
His Asp Leu Ile Gly Gly Lys Thr Val Ser Leu Asn Gln Asp Leu Thr	
610 615 620	
CTT CAG CCC TAT CAG GTC ATG TGG CTC GAA ATC GCC TGA CGCAGCTTC	2877
Leu Gln Pro Tyr Gln Val Met Trp Leu Glu Ile Ala *	
625 630 635	
CCAAATGCCG TCTGAACCGT TTCAGACGGC ATTTGCG	2914

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Leu Thr Pro Thr Gln Gln Val Gly Leu Ile Leu Gln Tyr Leu Lys	
1 5 10 15	
Thr Arg Ile Leu Asp Ile Tyr Thr Pro Glu Gln Arg Ala Gly Ile Glu	
20 25 30	
Lys Ser Glu Asp Trp Arg Gln Phe Ser Arg Arg Met Asp Thr His Phe	
35 40 45	
Pro Lys Leu Met Asn Glu Leu Asp Ser Val Tyr Gly Asn Asn Glu Ala	
50 55 60	
Leu Leu Pro Met Leu Glu Met Leu Leu Ala Gln Ala Trp Gln Ser Tyr	

65	70	75	80
Ser Gln Arg Asn Ser Ser Leu Lys Asp Ile Asp Ile Ala Arg Glu Asn	85	90	95
Asn Pro Asp Trp Ile Leu Ser Asn Lys Gln Val Gly Gly Val Cys Tyr	100	105	110
Val Asp Leu Phe Ala Gly Asp Leu Lys Gly Leu Lys Asp Lys Ile Pro	115	120	125
Tyr Phe Gln Glu Leu Gly Leu Thr Tyr Leu His Leu Met Pro Leu Phe	130	135	140
Lys Cys Pro Glu Gly Lys Ser Asp Gly Gly Tyr Ala Val Ser Ser Tyr	145	150	155
Arg Asp Val Asn Pro Ala Leu Gly Thr Ile Gly Asp Leu Arg Glu Val	165	170	175
Ile Ala Ala Leu His Glu Ala Gly Ile Ser Ala Val Val Asp Phe Ile	180	185	190
Phe Asn His Thr Ser Asn Glu His Glu Trp Ala Gln Arg Cys Ala Ala	195	200	205
Gly Asp Pro Leu Phe Asp Asn Phe Tyr Tyr Ile Phe Pro Asp Arg Arg	210	215	220
Met Pro Asp Gln Tyr Asp Arg Thr Leu Arg Glu Ile Phe Pro Asp Gln	225	230	235
His Pro Gly Gly Phe Ser Gln Leu Glu Asp Gly Arg Trp Val Trp Thr	245	250	255
Thr Phe Asn Ser Phe Gln Trp Asp Leu Asn Tyr Ser Asn Pro Trp Val	260	265	270
Phe Arg Ala Met Ala Gly Glu Met Leu Phe Leu Ala Asn Leu Gly Val	275	280	285
Asp Ile Leu Arg Met Asp Ala Val Ala Phe Ile Trp Lys Gln Met Gly	290	295	300
Thr Ser Cys Glu Asn Leu Pro Gln Ala His Ala Leu Ile Arg Ala Phe	305	310	315
Asn Ala Val Met Arg Ile Ala Ala Pro Ala Val Phe Phe Lys Ser Glu	325	330	335
Ala Ile Val His Pro Asp Gln Val Val Gln Tyr Ile Gly Gln Asp Glu	340	345	350
Cys Gln Ile Gly Tyr Asn Pro Leu Gln Met Ala Leu Leu Trp Asn Thr	355	360	365
Leu Ala Thr Arg Glu Val Asn Leu Leu His Gln Ala Leu Thr Tyr Arg	370	375	380

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His Asn Leu Pro Glu His Thr Ala Trp Val Asn Tyr Val Arg Ser His
385                      390                      395                      400

Asp Asp Ile Gly Trp Thr Phe Ala Asp Glu Asp Ala Ala Tyr Leu Gly
                      405                      410                      415

Ile Ser Gly Tyr Asp His Arg Gln Phe Leu Asn Arg Phe Phe Val Asn
                      420                      425                      430

Arg Phe Asp Gly Ser Phe Ala Arg Gly Val Pro Phe Gln Tyr Asn Pro
                      435                      440                      445

Ser Thr Gly Asp Cys Arg Val Ser Gly Thr Ala Ala Ala Leu Val Gly
                      450                      455                      460

Leu Ala Gln Asp Asp Pro His Ala Val Asp Arg Ile Lys Leu Leu Tyr
465                      470                      475                      480

Ser Ile Ala Leu Ser Thr Gly Gly Leu Pro Leu Ile Tyr Leu Gly Asp
                      485                      490                      495

Glu Val Gly Thr Leu Asn Asp Asp Asp Trp Ser Gln Asp Ser Asn Lys
                      500                      505                      510

Ser Asp Asp Ser Arg Trp Ala His Arg Pro Arg Tyr Asn Glu Ala Leu
                      515                      520                      525

Tyr Ala Gln Arg Asn Asp Pro Ser Thr Ala Ala Gly Gln Ile Tyr Gln
                      530                      535                      540

Gly Leu Arg His Met Ile Ala Val Arg Gln Ser Asn Pro Arg Phe Asp
545                      550                      555                      560

Gly Gly Arg Leu Val Thr Phe Asn Thr Asn Asn Lys His Ile Ile Gly
                      565                      570                      575

Tyr Ile Arg Asn Asn Ala Leu Leu Ala Phe Gly Asn Phe Ser Glu Tyr
                      580                      585                      590

Pro Gln Thr Val Thr Ala His Thr Leu Gln Ala Met Pro Phe Lys Ala
                      595                      600                      605

His Asp Leu Ile Gly Gly Lys Thr Val Ser Leu Asn Gln Asp Leu Thr
                      610                      615                      620

Leu Gln Pro Tyr Gln Val Met Trp Leu Glu Ile Ala *
625                      630                      635

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(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria polysaccharea*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTCACCATGG GCATCTTGGA CATC

24

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria polysaccharea*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CTGCCATGGT TCAGACGGCA TTTGG

25

Neisseria polysaccharea